AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1.-15. (Canceled)

16. (Currently Amended) A method for identifying a small molecule that binds to a target RNA, said method comprising:

(a) contacting a target RNA molecule with a library of small molecules under conditions that permit direct binding of the target RNA to a member of the library of small molecules and the formation of a target RNA:compound complex, wherein the target RNA is a region of human 28S rRNA, or RNA ~~contains~~ containing a premature stop codon that is in the context of UAAG, UAAA, UAGG, UAGC, UAGU, UAAC, UGAC, or UAAU; and

(b) detecting the formation of a target RNA:small molecule complex, wherein a small molecule that binds to the target RNA is identified if a target RNA:small molecule complex is detected.

17. (Currently Amended) A method of identifying a small molecule that modulates premature translation termination or nonsense-mediated mRNA decay, said method comprising:

(a) contacting a target RNA molecule with a library of small molecules under conditions that permit direct binding of the target RNA to a member of the library of small molecules and the formation of a target RNA:compound complex, wherein the target RNA is a region of human 28S rRNA, or RNA ~~contains~~ containing a premature stop codon that is in the context of UAAG, UAAA, UAGG, UAGC, UAGU, UAAC, UGAC, or UAAU;

(b) detecting the formation of a target RNA:small molecule complex, wherein a small molecule that binds to the target RNA is identified if a target RNA:small molecule complex is detected;

(c) contacting the small molecule identified as binding to a region of human 28S rRNA or a RNA containing a premature stop codon with a cell containing a nucleic acid sequence comprising a regulatory

element operably linked to a reporter gene, wherein the reporter gene comprises a premature stop codon; and

(d) detecting the protein expressed from the reporter gene, wherein a small molecule that modulates premature translation termination or nonsense-mediated mRNA decay is identified if the protein expressed from the reporter gene in the presence of the small molecule is altered relative to the protein expressed from the reporter gene in the absence of the small molecule or the presence of a negative control.

18. (Currently Amended) A method of identifying a small molecule that modulates premature translation termination or nonsense-mediated mRNA decay, said method comprising:

(a) contacting a target RNA molecule with a library of small molecules under conditions that permit direct binding of the target RNA to a member of the library of small molecules and the formation of a target RNA:compound complex, wherein the target RNA is a region of human 28S rRNA, or RNA ~~contains~~ containing a premature stop codon that is in the context of UAAG, UAAA, UAGG, UAGC, UAGU, UAAC, UGAC, or UAAU;

(b) detecting the formation of a target RNA:small molecule complex, wherein a small molecule that binds to the target RNA is identified if a target RNA:small molecule complex is detected;

(c) contacting the small molecule identified as binding to a region of human 28S rRNA or a RNA containing a premature stop codon with a cell-free extract and a nucleic acid sequence comprising a regulatory element operably linked to a reporter gene, wherein the reporter gene comprises a premature stop codon; and

(d) detecting the protein expressed from the reporter gene, wherein a small molecule that modulates premature translation termination or nonsense-mediated mRNA decay is identified if the protein expressed from the reporter gene in the presence of the small molecule is altered relative to the protein expressed from the reporter gene in the absence of the compound or the presence of a negative control.

19. (Previously Presented) The method of claim 16, 17 or 18 wherein the target RNA is detectably labeled.

20. (Previously Presented) The method of claim 16, 17 or 18, wherein the small molecules in the library are detectably labeled.

21. (Previously Presented) The method of claim 17, wherein the cell is a hybridoma cell, a pre-B cell, a 293 cell, a 293T cell, a HeLa cell, a HepG2 cell, a K562 cell, or a 3T3 cell.

22. (Previously Presented) The method of claim 18, wherein the cell-free extract is from human cells.

23. (Previously Presented) The method of claim 18, wherein the cell-free extract is rabbit reticulocyte lysate or wheat germ extract.

24. (Previously Presented) The method of claim 18, wherein the cell-free extract is a cell free extract from HeLa cells.

25. (Previously Presented) The method of claim 18 or 22, wherein the cell-free extract is isolated from cells that have been incubated on ice at least 12 hours.

26. (Previously Presented) The method of claim 18 or 22, wherein the cell-free extract is isolated from cells that have been incubated on ice at least 24 hours.

27. (Previously Presented) The method of claim 18 or 22, wherein the cell-free extract is a S10 to S30 cell-free extract.

28. (Previously Presented) The method of claim 25, wherein the cell-free extract is a S10 to S30 cell-free extract.

29. (Previously Presented) The method of claim 26, wherein the cell-free extract is a S10 to S30 cell-free extract.

30. (Previously Presented) The method of claim 18 or 22, wherein the cell-free extract is a S5 to S25 cell-free extract.

31. (Previously Presented) The method of claim 25, wherein the cell-free extract is a S5 to S25 cell-free extract.

32. (Previously Presented) The method of claim 26, wherein the cell-free extract is a S5 to S25 cell-free extract.

33. (Previously Presented) The method of claim 30, wherein the cell-free extract is a S10 cell-free extract.

34. (Previously Presented) The method of claim 31, wherein the cell-free extract is a S10 cell-free extract.

35. (Previously Presented) The method of claim 32, wherein the cell-free extract is a S10 cell-free extract.

36. (Currently Amended) The method of claim 16, 17 or 18, wherein the ~~28S rRNA~~ target RNA is human 28S rRNA.

37. (Currently Amended) The method of claim 16, 17 or 18, wherein the region of human 28S rRNA comprises a region involved in frameshifting, nonsense mutation suppression, GTPase activity, or peptidyl transferase activity.

38. (Previously Presented) The method of claim 16, 17, or 18, wherein each small molecule in the library is attached to a solid support.

39. (Previously Presented) The method of claim 38, wherein the solid support is a silica gel, a resin, a derivatived plastic film, a glass bead, cotton, a plastic bead, a polystyrene bead, an aluminum gel, a glass slide or a polysaccharide.

40. (Previously Presented) The method of claim 16, 17 or 18, wherein the library of small molecules is attached to a chip.

41. (Previously Presented) The method of claim 19, wherein the detectably labeled target RNA is labeled with a fluorescent dye, phosphorescent dye, ultraviolet dye, infrared dye, visible dye, radiolabel, enzyme, spectroscopic colorimetric label, affinity tag, or nanoparticle.

42. (Previously Presented) The method of claim 20, wherein the detectably labeled small molecules in the library are labeled with a fluorescent dye, phosphorescent dye, ultraviolet dye, infrared dye, visible dye, radiolabel, enzyme, spectroscopic colorimetric label, affinity tag, or nanoparticle.

43. (Previously Presented) The method of claim 16, 17 or 18, wherein the small molecule library is a library of benzodiazepines, isoprenoids, thiazolidinones, metathiazanones, pyrrolidines, morpholino compounds, or diazepindiones.

44. (Previously Presented) The method of claim 16, 17 or 18, wherein the detectably labeled target RNA:compound complex is detected by electrophoresis, fluorescence

spectroscopy, surface plasmon resonance, mass spectrometry, scintillation, proximity assay, structure-activity relationships ("SAR") by NMR spectroscopy, size exclusion chromatography, affinity chromatography, or nanoparticle aggregation.

45. (Previously Presented) The method of claim 16, 17 or 18, wherein the method further comprises determining the structure of the compound.

46. (Previously Presented) The method of claim 45, wherein the structure of the compound is determined by mass spectroscopy, NMR, X-ray crystallography, Edman degradation or vibration spectroscopy.

47. (Previously Presented) The method of claim 16, 17 or 18, wherein the premature stop codon is UAG, UGA or UAA.

48. (Currently Amended) The method of claim 16, 17 or 18, wherein the target RNA is RNA containing a premature stop codon that is in the context ~~is~~ of UAAG, UAAA, UAGG, UAGC, UAGU, UAAC, UGAC, ~~UGAG~~ or UAAU.

49. (Previously Presented) The method of claim 17 or 18, wherein the reporter gene contains 2 or more premature stop codons.

50. (Previously Presented) The method of claim 17 or 18, wherein an increase in the amount of protein expressed in the presence of the small molecule relative to the amount of protein expressed in the absence of the small molecule or the presence of a negative control indicates that the small molecule suppresses premature translation termination or nonsense-mediated mRNA decay.

51. (Previously Presented) The method of claim 17 or 18, wherein a decrease in the amount of protein expressed in the presence of the small molecule relative to the amount of protein expressed in the absence of the small molecule or the presence of a negative control indicates that the small molecule enhances premature translation termination or nonsense-mediated mRNA decay.